

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO:1: MTB32A (Ra35 FL)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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15 GACTACGTTG GTGTAGAAAA ATCCTGCCGC CCGGACCCTT AAGGCTGGGA CAATTTCTGA      60
   TAGCTACCCC GACACAGGAG GTTACGGGAT GAGCAATTCG CGCCGCCGCT CACTCAGGTG      120
   GTCATGGTTG CTGAGCGTGC TGGCTGCCGT CGGGCTGGGC CTGGCCACGG CGCCGGCCCA      180
   GCGCGCCCCG CCGGCTTGT CGCAGGACCG GTTCGCCGAC TTCCCCGCGC TGCCCCCTCGA      240
   CCCGTCCGCG ATGGTCGCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAAGTGGG      300
20 CTACAACAAC GCCGTGGGCG CCGGGACCGG CATCGTCATC GATCCCAACG GTGTCTGTCT      360
   GACCAACAAC CACGTGATCG CCGGCGCCAC CGACATCAAT GCGTTCAGCG TCGGCTCCGG      420
   CCAAACCTAC GGCCTCGATG TGGTCGGGTA TGACCGCACC CAGGATGTCT CCGTGCTGCA      480
   GCTGCGCGGT GCCGTGGGCC TGCCGTCCGC GGCATCGGT GCGGCGCTCG CCGTTGGTGA      540
   GCCCGTCGTC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACGCCCCGTG CCGTGCCTGG      600
25 CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GCGCTCGGAT TCGTGACCG GTGCCGAAGA      660
   GACATTGAAC GGGTTGATCC AGTTCGATGC CGCAATCCAG CCCGGTGATT CCGGCGGGCC      720
   CGTCGTCAAC GGCCTAGGAC AGGTGGTCGG TATGAACACG GCCCGGTCCG ATAACCTCCA      780
   GCTGTCCAG GGTGGGCAGG GATTCCGCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG      840
   CCAAAATCCGA TCGGTGGGG GGTACCCAC CGTTCATATC GGGCCTACCG CCTTCCTCGG      900
30 CTTGGGTGTT GTCGACAACA ACGGCAACGG CGCAGAGTC CAACGCGTGG TCGGAAGCGC      960
   TCCGGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC ACCGCGGTCT ACGGCGCTCC      1020
   GATCAACTCG GCCACCGCGA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCTAT      1080
   CTCGGTGAAC TGGCAAACCA AGTCGGGCGG CACGCGTACA GGAACGTGA CATTGGCCGA      1140
   GGGACCCCGG GCCTGATTTG TCGCGGATAC CACCCGCCCG CCGGCAATT GGATTGGCGC      1200
35 CAGCCGTGAT TGCCCGGTGA GCCCCGAGT TCCGTCTCCC GTGCGCGTGG CATTGTGGAA      1260
   GCAATGAACG AGGCAGAACA CAGCGTTGAG CACCCTCCCG TGCAGGGCAG TTACGTCGAA      1320
   GGCGGTGTGG TCGAGCATCC GGATGCCAAG GACTTCGGCA GCGCCGCCGC CCTGCCCGCC      1380
   GATCCGACCT GGTTTAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC      1440
   GCCAGCGCGG ACGGTTCCGN CGATCTGCGT GGACTCATCG ATCGCTCGA CTACCTGCAG      1500
40 TGGCTTGCCA TCGACTGCAT CTGTTGCCGC GTTCTTACG ACTCACCGCT GCGCGACGGC      1560
   GGTTACGACA TTCGCGACTT CTACAAGGTG TCGCCGAAT TCGGCACCGT CGACGATTTC      1620
   GTCGCCCTGG TCGACACCGC TCACCGCGCA GGTATCCGCA TCATCACCGA CCTGGTGATG      1680
   AATCACACCT CGGAGTCGCA CCCCTGGTTT CAGGAGTCCC GCGCGACCC AGACGGACCG      1740
45 TACGGTGAAT ATTACGTGTG GAGCGACACC AGCGAGCGCT ACACCGACGC CCGGATCATC      1800
   TTCGTCGACA CCGAAGAGTC GAACTGGTCA TTGATCTCTG TCCGCCGACA GTTNCCTACTG      1860
   GCACCGATTTC TT
1872

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: MTB32A (Ra35FL)

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60 Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
   1           5           10           15
   Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
   20           25           30
   Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
   35           40           45
65 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
   50           55           60
   Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
   65           70           75           80

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	Phe	Ala	Asp	Phe 20	Pro	Ala	Leu	Pro	Leu 25	Asp	Pro	Ser	Ala	Met	Val	Ala
5	Gln	Val	Gly 35	Pro	Gln	Val	Val	Asn 40	Ile	Asn	Thr	Lys	Leu 45	Gly	Tyr	Asn
	Asn	Ala	Val	Gly	Ala	Gly	Thr 55	Gly	Ile	Val	Ile	Asp 60	Pro	Asn	Gly	Val
10	Val	Leu	Thr	Asn	Asn	His 70	Val	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala 80
15	Phe	Ser	Val	Gly	Ser 85	Gly	Gln	Thr	Tyr	Gly 90	Val	Asp	Val	Val	Gly 95	Tyr
	Asp	Arg	Thr	Gln 100	Asp	Val	Ala	Val	Leu 105	Gln	Leu	Arg	Gly	Ala 110	Gly	Gly
20	Leu	Pro	Ser 115	Ala	Ala	Ile	Gly	Gly 120	Gly	Val	Ala	Val	Gly 125	Glu	Pro	Val
	Val	Ala	Met	Gly	Asn	Ser	Gly 135	Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val
25	Pro	Gly	Arg	Val	Val	Ala 150	Leu	Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser 160
30	Leu	Thr	Gly	Ala 165	Glu	Glu	Thr	Leu	Asn	Gly 170	Leu	Ile	Gln	Phe	Asp 175	Ala
	Ala	Ile	Gln	Pro 180	Gly	Asp	Ser	Gly	Gly 185	Pro	Val	Val	Asn	Gly	Leu	Gly
35	Gln	Val	Val 195	Gly	Met	Asn	Thr	Ala 200	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser
	Gln	Gly	Gly 210	Gln	Gly	Phe	Ala 215	Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile
40	Ala	Gly	Gln	Ile	Arg	Ser 230	Gly	Gly	Gly	Ser	Pro 235	Thr	Val	His	Ile	Gly 240
45	Pro	Thr	Ala	Phe	Leu 245	Gly	Leu	Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly 255
	Ala	Arg	Val	Gln 260	Arg	Val	Val	Gly	Ser 265	Ala	Pro	Ala	Ala	Ser	Leu	Gly
50	Ile	Ser	Thr 275	Gly	Asp	Val	Ile	Thr 280	Ala	Val	Asp	Gly	Ala 285	Pro	Ile	Asn
	Ser	Ala	Thr 290	Ala	Met	Ala	Asp 295	Ala	Leu	Asn	Gly	His 300	His	Pro	Gly	Asp
55	Val	Ile	Ser	Val	Thr	Trp 310	Gln	Thr	Lys	Ser	Gly 315	Gly	Thr	Arg	Thr	Gly 320
60	Asn	Val	Thr	Leu	Ala 325	Glu	Gly	Pro	Pro	Ala 330						

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65      <212> DNA
      <213> Ra35FLMutSA
      <400> SEQ ID NO:5

      catatcgcatc accatcacca tcacgcccgc ccggccttgt cgcaggaccg gttcgccgac 60
      ttccccgcgc tgcctctcga ccggtccgcg atggtcgccc aagtgggggc acaggtggtc 120
      aacatcaaca ccaaactggg ctacaacaac gccgtggggc cggggaccgg catcgtcac 180

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gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcgccac cgacatcaat 240
gcgttcagcg tcggctccgg ccaaacctac ggcgtcgatg tggtcgggta tgaccgcacc 300
caggatgtcg cgggtgctgca gctgcgcggt gccggtggcc tgccgtcggc ggcgatcgg 360
ggcggcgctcg cgggttggtga gcccgtcgtc gcgatgggca acagcgggtg gcagggcgga 420
5 acgccccgtg cgggtgcctgg caggggtggtc gcgctcggcc aaaccgtgca ggcgtcggat 480
tcgctgaccg gtgccgaaga gacattgaac gggttgatcc agttcgatgc cgcgatccag 540
cccggtgatg cgggcgggcc cgtcgtcaac ggcctaggac aggtgggtcgg tatgaacacg 600
ggcgcgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggg 660
10 caggcgatgg cgatcgcggg ccagatccga tcgggtgggg ggtcaccac cgttcatac 720
gggctaccg ccttcctcgg cttgggtgtt gtcgacaaca acggcaacgg cgcacgagtc 780
caacgcgtgg tcgggagcgc tccggcgga agtctcggca tctccaccgg cgacgtgatc 840
accgcggtcg acggcgctcc gatcaactcg gccaccgcga tggcggacgc gcttaacggg 900
catcatcccg gtgacgtcat ctcggtgacc tggcaacca agtcgggcgg cagcgtaca 960
15 gggaacgtga cattggccga gggacccccg gcctgagaat tc 1002

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<212> PRT
<213> Ra35FLMutSA
<400> SEQ ID NO:6

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20 Met His His His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
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25 Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
      20 25 30

Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
      35 40 45

30 Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
      50 55 60

Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
      65 70 75 80

35 Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
      85 90 95

40 Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
      100 105 110

Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val
      115 120 125

45 Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
      130 135 140

Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
      145 150 155 160

50 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
      165 170 175

Ala Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly
      180 185 190

55 Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
      195 200 205

60 Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
      210 215 220

Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly
      225 230 235 240

65 Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
      245 250 255

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Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
 260 265 270
 5 Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
 275 280 285
 Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
 290 295 300
 10 Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
 305 310 315 320
 Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 325 330
 15

(2) INFORMATION FOR SEQ ID NO:7: Ra35 (MTB32A N-term)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

gccccgcggccttgctgcaggaccgggttcgccgacttccccgcgctgcccctcgaccggtccgcg
 atgggtcgcccaagtggggccacaggtgggtcaacatcaacaccaaactgggctacaacaacgcggtg
 30 ggcgcgggaccggcatcgatcgatcccaacgggtgctgctgacctacaaccacgtgatcgcg
 ggccgacacatcaatgcgttcagcgctcggtccggccaaacctacggcgctcgatgtgggtcggg
 tatgaccgcacccaggatgtcgcggtgctgcagctgcgcggtgcccgtggcctgcccgtcgccggtg
 atcggtggcggtcggtggtgagcccgctcgctcgatgggcaacagcggtgggcaggcgga
 acgccccgtgcgggtgctggcagggtgggtcgcgctcgcccaaaccgtgcaggcgctcggttcgctg
 35 accggtgcccgaagagacattgaacgggtgatccagttcgatgccgcgatccagccccgtgagggc
 ggccgggcccgtcgctcaacggcctaggacaggtgggtcggtatgaacacggccgcgctcc

(2) INFORMATION FOR SEQ ID NO:8: Ra35 (MTB32A N-term)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 50 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 55 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 60 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 65 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
Ala Ala Ser

5

(2) INFORMATION FOR SEQ ID NO:9: Ra12

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGTATGAAC ACGGCCGCGT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTTCG 60
CATTCGGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC 120
CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTCGACA ACAACGGCAA 180
CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC 240
CGGCGACGTG ATCACC GCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA 300
CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAA CCAAGTCGGG 360
CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TTCGTCGYGG 420
ATACCACCCG CCGGCCGGCC AATTGGA 447

25

(2) INFORMATION FOR SEQ ID NO:10: Ra12

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20 25 30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35 40 45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50 55 60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65 70 75 80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 90 95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100 105 110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115 120 125
Gly Pro Pro Ala
130

55

(2) INFORMATION FOR SEQ ID NO:11: TbH9

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGCAGGGTG GCGTGGATGA GCGTCACCGC GGGGCAGGCC GAGCTGACCG CCGCCCAGGT 60
CCGGTTTGCT GCGGCGGCCT ACGAGACGGC GTATGGGCTG ACGGTGCCCC CGCCGGTGAT 120

CGCCGAGAAC CGTGCTGAAC TGATGATTCT GATAGCGACC AACCTCTTGG GGCAAAACAC 180
 CCCGGCGATC GCGGTCAACG AGGCCGAATA CGGCGAGATG TGGGCCCAAG ACGCCGCCGC 240
 GATGTTTGGC TACGCCGCGG CGACGGCGAC GGCGACGGCG ACGTTGCTGC CGTTCGAGGA 300
 5 GGCGCCGGAG ATGACCAGCG CGGGTGGGCT CCTCGAGCAG GCCGCCGCGG TCGAGGAGGC 360
 CTCCGACACC GCCGCGGCGA ACCAGTTGAT GAACAATGTG CCCCAGGCGC TGAACAGTT 420
 GGCCAGCCC ACGCAGGGCA CCACGCCTTC TTCCAAGCTG GGTGGCCTGT GGAAGACGGT 480
 CTCGCCGCAT CGGTCGCCGA TCAGCAACAT GGTGTCGATG GCCAACAACC ACATGTCGAT 540
 GACCAACTCG GGTGTGTCGA TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTCC 600
 10 GGCGGCGGCC GCCCAGGCCG TGCAAACCGC GGCGCAAAAC GGGGTCCGGG CGATGAGCTC 660
 GCTGGGCAGC TCGCTGGGTT CTTGCGGTCT GGGCGGTGGG GTGGCCGCCA ACTTGGGTCG 720
 GGCGGCCTCG GTACGGTATG GTCACCGGGA TGGCGGAAAA TATGCANAGT CTGGTCGGCG 780
 GAACGGTGGT CCGGCGTAAG GTTTACCCCC GTTTTCTGGA TGCGGTGAAC TTCGTCAACG 840
 GAAACAGTTA C 851

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 amino acids
 20 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: TbH9

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Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 1 5 10 15
 Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 20 25 30
 30 Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 35 40 45
 Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 50 55 60
 35 Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
 65 70 75 80
 Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
 85 90 95
 Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
 100 105 110
 40 Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
 115 120 125
 Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
 130 135 140
 45 Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
 145 150 155 160
 His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
 165 170 175
 Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
 180 185 190
 50 Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
 195 200 205
 Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
 210 215 220
 55 Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
 225 230 235 240
 Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
 245 250 255
 Arg Arg Asn Gly Gly Pro Ala
 260

60

(2) INFORMATION FOR SEQ ID NO:13: TBH9FL

(i) SEQUENCE CHARACTERISTICS:
 65 (A) LENGTH: 3058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5	GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT	60
	GGCATACCCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC	120
	TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA	180
10	TGAGGTGTCG GCGCTGACTG CGGCGCACTT CGCCGCACAT GCGGCGATGT ATCAGTCCGT	240
	GAGCGCTCGG GCTGCTGCGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG	300
	CTCGTATGCG GCCACTGAAG TCGCCAATGC GCGGCGGCC AGCTAAGCCA GGAACAGTCG	360
15	GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGGA TTTCGGGGCG TTACCACCGG	420
	AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC CTCGCTGGTG GCCGCGGCTC	480
20	AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC GTCGGCGTTT CAGTCGGTGG	540
	TCTGGGGTCT GACGGTGGGG TCGTGATAG GTTCGTCGGC GGGTCTGATG GTGGCGGCGG	600
	CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA GGCCGAGCTG ACCGCCGCC	660
25	AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG GCTGACGGTG CCCCCGCCG	720
	TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA	780
30	ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGCGA GATGTGGGCC CAAGACGCCG	840
	CCGCGATGTT TGGCTACGCC GCGGCGACGG CGACGGCGAC GGCGACGTTG CTGCCGTTG	900
	AGGAGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC GCGGTCGAGG	960
35	AGGCCTCCGA CACCGCCGCG GCGAACCAGT TGATGAACAA TGTGCCCCAG GCGCTGCAAC	1020
	AGCTGGCCCA GCCCACGAG GGCACCACGC CTTCTTCCAA GCTGGGTGGC CTGTGGAAGA	1080
40	CGGTCTCGCC GCATCGGTCG CCGATCAGCA ACATGGTGTC GATGGCCAAAC AACCACATGT	1140
	CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGGCTTTG	1200
	CTCCGGCGGC GGCCGCCCAG GCCGTGCAAA CCGCGGCGCA AAACGGGGTC CGGGCGATGA	1260
45	GCTCGCTGGG CAGCTCGCTG GGTCTTTCGG GTCTGGGCGG TGGGTGGCC GCCAACTTGG	1320
	GTCGGGCGGC CTCGGTCGGT TCGTTGTTCG TGCCGCAGGC CTGGGCCGCG GCCAACCAGG	1380
50	CAGTCACCCC GCGGCGCGCG GCGCTGCCGC TGACCAGCCT GACCAGCGCC GCGGAAAGAG	1440
	GGCCCCGGCA GATGCTGGGC GGGCTGCCGG TGGGGCAGAT GGGCGCCAGG GCCGCTGGTG	1500
	GGCTCAGTGG TGTGCTGCGT GTTCCGCCGC GACCCTATGT GATGCCGCAT TCTCCGGCGG	1560
55	CCGGCTAGGA GAGGGGGCGC AGACTGTCGT TATTTGACCA GTGATCGGCG GTCTCGGTGT	1620
	TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG	1680
60	GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTTATG ACGGATCCGC ACGCGATGCG	1740
	GGACATGGCG GGCCGTTTGG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGGAT	1800
	GTGGGCGTCC GCGCAAAACA TTTCGGGTGC GGGCTGGAGT GGCATGGCCG AGGCGACCTC	1860
65	GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGCTGCACGG	1920
	GGTGCGTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA	1980

GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAAT ACTTTTACAA GCGAAGGAGA 2040
 5 ACAGGTTCGA TGACCATCAA CTATCAATTC GGGGATGTCG ACGCTCACGG CGCCATGATC 2100
 CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTCTGTA TGTGTTGACC 2160
 GCGAGTGACT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTTCAT TACCCAGTTG 2220
 10 GGCCGTAAC TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT 2280
 GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGGC CTGACACCAG 2340
 15 GCCAAGGCCA GGGACGTGGT GTACGAGTGA AGTTCCTCGC GTGATCCTTC GGGTGGCAGT 2400
 CTAAGTGGTC AGTGCTGGGG TGTGTTGGT TTGCTGCTTG GCGGGTTCCTT CGGTGCTGGT 2460
 CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCCAGG TAGCGCCGTC CTTGATCCA 2520
 20 TTCGTCGTGT TGTTCGGCGA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCGGG 2580
 GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT 2640
 25 GTTGACCAG ATTTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT 2700
 GCGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC 2760
 CCGATCATAT TGGGCAACAA CTGATTCGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG 2820
 30 GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG 2880
 GGTTCCTGCAG CGCTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCGG CCACCAGGCC 2940
 GGCGTGGGCG TCGCTGGTGA CCAGCGCGAC CCCGACAGG CCGCGGGCGA CCAGGTCGCG 3000
 35 GAAGAACGCC AGCCAGCCGG CCCCGTCCTC GGCGGAGGTG ACCTGGATGC CCAGGATC 3058

(2) INFORMATION FOR SEQ ID NO:14: TbH9FL

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
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 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
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 Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
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 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
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 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
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 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
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Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
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 5 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
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 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
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 10 Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
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 Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190
 15 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
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 20 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 25 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 35 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
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 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 40 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
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 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
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 Pro His Ser Pro Ala Ala Gly
 385 390

55

<210> SEQ ID NO:15
 <211> 2287
 <212> DNA
 <213> Artificial Sequence
 <223> Description of Artificial Sequence:tri-fusion
 protein Mtb72F(Ra12-TbH9-Ra35 or Mtb32-Mtb39
 fusion)

60

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 Met His His His His
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	Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile	
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10	cga tcg ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc	200
	Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe	
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15	ctc ggc ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa	248
	Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln	
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	Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly	
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	Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala	
	90 95 100	
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	Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val	
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	Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu	
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	Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro	
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	Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser	
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	Leu Val Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe	
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	Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly	
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	Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala	
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70	gcc cag gtc ccg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg	776
	Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu	
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75	acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att	824
	Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile	
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	Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val	
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25	ccg Pro	cat His	cgg Arg	tcg Ser	ccg Pro	atc Ile	agc Ser	aac Asn	atg Met	gtg Val	tcg Ser	atg Met	gcc Ala	aac Asn	aac Asn	cac His	1208
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35	atg Met	ttg Leu	aag Lys	ggc Gly	ttt Phe	gct Ala	ccg Pro	gcg Ala	gcg Ala	gcc Ala	cgc Arg	cag Gln	gcc Ala	gtg Val	caa Gln	acc Thr	1304
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45	gcc Ala	tcg Ser	gtc Val	ggc Gly	tcg Ser	ttg Leu	tcg Ser	gtg Val	ccg Pro	cag Gln	gcc Ala	tgg Trp	gcc Ala	gcg Ala	gcc Ala	aac Asn	1448
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		470				475					480					485	
55	agc Ser	gcc Ala	gcg Ala	gaa Glu	aga Arg	ggg Gly	ccc Pro	ggg Gly	cag Gln	atg Met	ctg Leu	ggc Gly	ggg Gly	ctg Leu	ccg Pro	gtg Val	1544
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20	caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val 615 620 625	1928
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40	ctc ggc caa acc gtg cag gcg tgc gat tgc ctg acc ggt gcc gaa gag Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu 680 685 690	2120
45	aca ttg aac ggc ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp 695 700 705	2168
50	tcg ggc ggc ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn 710 715 720 725	2216
55	acg gcc gcg tcc taggatatcc atcacactgg cggccgctcg agcagatccg Thr Ala Ala Ser	2268
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75	Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala 20 25 30	
80	Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile 35 40 45	
85	Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	

		50				55				60							
5		Gly 65	Ala	Arg	Val	Gln	Arg 70	Val	Val	Gly	Ser	Ala 75	Pro	Ala	Ala	Ser	Leu 80
		Gly	Ile	Ser	Thr	Gly 85	Asp	Val	Ile	Thr	Ala 90	Val	Asp	Gly	Ala	Pro 95	Ile
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25		Gly	Leu	Thr 195	Val	Gly	Ser	Trp	Ile 200	Gly	Ser	Ser	Ala 205	Gly	Leu	Met	Val
		Ala 210	Ala	Ala	Ser	Pro	Tyr	Val 215	Ala	Trp	Met	Ser	Val 220	Thr	Ala	Gly	Gln
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35		Ala	Glu	Leu	Met 260	Ile	Leu	Ile	Ala	Thr 265	Asn	Leu	Leu	Gly	Gln 270	Asn	Thr
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		Ala 305	Thr	Leu	Leu	Pro	Phe 310	Glu	Glu	Ala	Pro	Glu 315	Met	Thr	Ser	Ala	Gly 320
45		Gly	Leu	Leu	Glu 325	Gln	Ala	Ala	Val	Glu 330	Glu	Ala	Ser	Asp	Thr 335	Ala	
		Ala	Ala	Asn	Gln 340	Leu	Met	Asn	Asn 345	Val	Pro	Gln	Ala	Leu 350	Gln	Gln	Leu
50		Ala	Gln	Pro 355	Thr	Gln	Gly	Thr	Thr 360	Pro	Ser	Ser	Lys 365	Leu	Gly	Gly	Leu
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55		Met 385	Ala	Asn	Asn	His	Met 390	Ser	Met	Thr	Asn	Ser 395	Gly	Val	Ser	Met	Thr 400
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[illegible]

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<210> SEQ ID NO:17
<211> 2190
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<210> SEQ ID NO:18
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10	Gly Leu Thr Val Gly	Ser Trp Ile Gly Ser Ser	Ala Gly Leu Met Val	195	200	205	
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15	Ala Glu Leu Thr Ala	Ala Gln Val Arg Val	Ala Ala Ala Tyr Glu	225	230	235	240
20	Thr Ala Tyr Gly Leu	Thr Val Pro Pro Pro	Val Ile Ala Glu Asn Arg	245	250	255	
	Ala Glu Leu Met Ile	Leu Ile Ala Thr Asn	Leu Leu Gly Gln Asn Thr	260	265	270	
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35	Gly Leu Leu Glu Gln	Ala Ala Ala Val Glu	Glu Ala Ser Asp Thr Ala	325	330	335	
	Ala Ala Asn Gln Leu	Met Asn Asn Val Pro	Gln Ala Leu Gln Gln Leu	340	345	350	
40	Ala Gln Pro Thr Gln	Gly Thr Thr Pro Ser	Ser Lys Leu Gly Gly Leu	355	360	365	
	Trp Lys Thr Val Ser	Pro His Arg Ser Pro	Ile Ser Asn Met Val Ser	370	375	380	
45	Met Ala Asn Asn His	Met Ser Met Thr Asn	Ser Gly Val Ser Met Thr	385	390	395	400
50	Asn Thr Leu Ser Ser	Met Leu Lys Gly Phe	Ala Pro Ala Ala Ala Ala	405	410	415	
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55	Leu Gly Ser Ser Leu	Gly Ser Ser Gly Leu	Gly Gly Val Ala Ala	435	440	445	
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20	Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp	
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	Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu	
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	Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro	
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	20 25 30	
	ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt	144
	Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe	
	35 40 45	
65	tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg	192
	Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly	
	50 55 60	

	tcg	tgg	ata	ggg	tcg	tcg	gcg	ggg	ctg	atg	gtg	gcg	gcc	tcg	ccg		240
	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	
	65					70					75				80		
5	tat	gtg	gcg	tgg	atg	agc	gtc	acc	gcg	ggg	cag	gcc	gag	ctg	acc	gcc	288
	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	
					85					90					95		
10	gcc	cag	gtc	cgg	gtt	gct	gcg	gcg	gcc	tac	gag	acg	gcg	tat	ggg	ctg	336
	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	
				100					105					110			
15	acg	gtg	ccc	ccg	ccg	gtg	atc	gcc	gag	aac	cgt	gct	gaa	ctg	atg	att	384
	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	
			115					120					125				
20	ctg	ata	gcg	acc	aac	ctc	ttg	ggg	caa	aac	acc	ccg	gcg	atc	gcg	gtc	432
	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	
		130					135					140					
25	aac	gag	gcc	gaa	tac	ggc	gag	atg	tgg	gcc	caa	gac	gcc	gcc	gcg	atg	480
	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	
	145					150					155					160	
30	ttt	ggc	tac	gcc	gcg	gcg	acg	gcg	acg	gcg	acg	gcg	acg	ttg	ctg	ccg	528
	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	
					165				170					175			
35	ttc	gag	gag	gcg	ccg	gag	atg	acc	agc	gcg	ggg	ggg	ctc	ctc	gag	cag	576
	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln	
				180					185				190				
40	gcc	gcc	gcg	gtc	gag	gag	gcc	tcc	gac	acc	gcc	gcg	gcg	aac	cag	ttg	624
	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	
			195					200					205				
45	atg	aac	aat	gtg	ccc	cag	gcg	ctg	caa	cag	ctg	gcc	cag	ccc	acg	cag	672
	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	Leu	Ala	Gln	Pro	Thr	Gln	
		210					215					220					
50	ggc	acc	acg	cct	tct	tcc	aag	ctg	ggg	ggc	ctg	tgg	aag	acg	gtc	tcg	720
	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser	
	225					230					235					240	
55	ccg	cat	cgg	tcg	ccg	atc	agc	aac	atg	gtg	tcg	atg	gcc	aac	aac	cac	768
	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser	Met	Ala	Asn	Asn	His	
					245					250					255		
60	atg	tcg	atg	acc	aac	tcg	ggg	gtg	tcg	atg	acc	aac	acc				

	cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc agc ctg acc	1056
	Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr	
	340 345 350	
5	agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg	1104
	Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val	
	355 360 365	
10	ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt	1152
	Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg	
	370 375 380	
15	gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat	1200
	Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp	
	385 390 395 400	
20	atc gcc ccg ccg gcc ttg tgc cag gac cgg ttc gcc gac ttc ccc gcg	1248
	Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala	
	405 410 415	
25	ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg	1296
	Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val	
	420 425 430	
30	gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg	1344
	Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly	
	435 440 445	
35	acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac	1392
	Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His	
	450 455 460	
40	gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc	1440
	Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly	
	465 470 475 480	
45	caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc	1488
	Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val	
	485 490 495	
50	gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tgc gcg gcg atc	1536
	Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile	
	500 505 510	
55	ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc	1584
	Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser	
	515 520 525	
60	ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg	1632
	Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	
	530 535 540	
65	ctc ggc caa acc gtg cag gcg tgc gat tgc ctg acc ggt gcc gaa gag	1680
	Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu	
	545 550 555 560	
70	aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat	1728
	Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	
	565 570 575	
75	tgc ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac	1776
	Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	
	580 585 590	
80	acg gcc gcg tcc taggatatc	1797
	Thr Ala Ala Ser	
	595	

<210> SEQ ID NO:20

<211> 596

<212> PRT

5 <213> Artificial Sequence

<223> Description of Artificial Sequence:bi-fusion
protein TbH9-Ra35 (designated Mtb59f)

10 His Met His His His His His His Met Val Asp Phe Gly Ala Leu Pro
1 5 10 15
Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
20 25 30
15 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
35 40 45
Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
50 55 60
20 Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
65 70 75 80
25 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
85 90 95
Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
100 105 110
30 Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
115 120 125
Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
130 135 140
35 Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
145 150 155 160
40 Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
165 170 175
Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
180 185 190
45 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
195 200 205
Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
210 215 220
50 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
225 230 235 240
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
245 250 255
55 Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
260 265 270
60 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr
275 280 285
Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
290 295 300
65 Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
305 310 315 320
Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn


```

ACAGTACATC GGCCTTGTCG AGTCGGTTGC CGGCTCCTGC AACAACTATT AAGCCCATGC      300
GGGCCCCATC CCGCGACCCG GCATCGTCGC CGGGGCTAGG CCAGATTGCC CCGCTCCTCA      360
ACGGGCGGCA TCCCGCGACC CGGCATCGTC GCCGGGGCTA GGCCAGATTG CCCCCTCCT      420
CAACGGGGCCG CATCTCGTGC CGAATTCCTG CAGCCCGGGG GATCCACTAG TTCTAGAGCG      480
5 GCCGCCACCG CGGTGGAGCT                                     500

```

(2) INFORMATION FOR SEQ ID NO:22: DPV (MTB8.4)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1          5          10          15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20        20        25        30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35        40        45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
25        50        55        60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65        70        75        80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85        90        95

```

(2) INFORMATION FOR SEQ ID NO:23: MSL (MTB9.8)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

TGGATTCCGA TAGCGGTTTC GGCCCCCTCGA CGGGCGACCA CGGCGCGCAG GCCTCCGAAC      60
GGGGGGCCGG GACGCTGGGA TTCGCCGGA CCGCAACCAA AGAACGCCGG GTCCGGGCGG      120
TCGGGCTGAC CGCACTGGCC GGTGATGAGT TCGGCAACGG CCCCCTGATG CCGATGGTGC      180
CGGGGACCTG GGAGCAGGGC AGCAACGAGC CCGAGGCGCC CGACGGATCG GGGAGAGGGG      240
GAGGCGACGG CTTACCGCAC GACAGCAAGT AACC GAATTC CGAATCACGT GGACCCGTAC      300
GGGTCGAAAG GAGAGATGTT ATGAGCCTTT TGGATGCTCA TATCCACAG TTGGTGGCCT      360
CCCAGTCGGC GTTTGCCGCC AAGGCGGGGC TGATGCGGCA CACGATCGGT CAGGCCGAGC      420
AGGCGGCGAT GTCGGCTCAG GCGTTTCACC AGGGGGAGTC GTCGGCGGCG TTTCAGGCCG      480
55 CCCATGCCCC GTTTGTGGCG GCGGCCGCCA AAGTCAACAC CTTGTTGGAT GTCGCGCAGG      540
CGAATCTGGG TGAGGCCGCC GGTACCTATG TGGCCGCCGA TGCTG                                     585

```

(2) INFORMATION FOR SEQ ID NO:24: MSL (MTB9.8)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1      5      10      15
5  Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
    20      25      30
    Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
      35      40      45
10  Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
    50      55      60
    Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
    65      70      75      80
    Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
      85      90      95
15  Phe

```

(2) INFORMATION FOR SEQ ID NO:25: MTI (MTB9.9A)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

CCGCTCTCTT TCAACGTCAT AAGTTCGGTG GGCCAGTCGG CCGCGCGTGC ATATGGCACC      60
AATAACGCGT GTCCCATGGA TACCCGGACC GCACGACGGT AGAGCGGATC AGCGCAGCCG      120
35  GTGCCGAACA CTACCGCGTC CACGCTCAGC CCTGCCGCGT TGCAGGAAGAT CGAGCCCAGG      180
    TTCTCATGGT CGTTAACGCC TTCCAACACT GCGACGGTGC GCGCCCCGGC GACCACCTGA      240
    GCAAACGCTCG GCTCCGGCAC CCGGCGCGCG GCTGCCAACA CCCCACGATT GAGATGGAAG      300
    CCGATCACCC GTGCCATGAC ATCAGCCGAC GCTCGATAGT ACGGCGCGCC GACACCGGCC      360
    AGATCATCCT TGAGCTCGGC CAGCCGGCGG TCGGTGCCGA ACAGCGCCAG CGGCGTGAAC      420
40  CGTGAGGCCA GCATGCGCTG CACCACCAGC ACACCTCGG CGATCACCAA CGCCTTGCCG      480
    GTCGGCAGAT CGGGACNACN GTCGATGCTG TTCAGGTCAC GGAAATCGTC GAGCCGTGGG      540
    TCGTCGGGAT CGCAGACGTC CTGAACATCG AGGCCGTCGG GGTGCTGGGC ACAACGGCCT      600
    TCGGTACCGG GCTTTCGTCG ACCAGAGCCA GCATCAGATC GGCGGCGCTG CGCAGGATGT      660
    CACGCTCGCT GCGGTTTCAG GTCGCGAGCC GCTCAGCCAG CCACTCTTGC AGAGAGCCGT      720
45  TGCTGGGATT AATTGGGAGA GGAAGACAGC ATGTCGTTTC TGACCACACA GCCGGAAGCC      780
    CTGGCAGCTG CGGCGGCGAA CCTACAGGGT ATTGGCACGA CAATGAACGC CCAGAACGCG      840
    GCCGCGGCTG CTCCAACCAC CGGAGTAGTG CCGCAGCCG CCGATGAAGT ATCAGCGCTG      900
    ACCGCGGCTC AGTTTGCTGC GCACGCGCAG ATGTACCAAA CGGTCAGCGC CCAGGCCGCG      960
50  GCCATTACAG AAATGTTCTG GAACACGCTG GTGGCCAGTT CTGGCTCATA CGCGGCCACC      1020
    GAGGCGGCCA ACGCAGCCGC TGCCGGCTGA ACGGGCTCGC ACGAACCTGC TGAAGGAGAG      1080
    GGGGAACATC CGGAGTTCTC GGGTCAGGGG TTGCGCCAGC GCCCAGCCGA TTCAGNTATC      1140
    GGCGTCCATA ACAGCAGACG ATCTAGGCAT TCAGTACTAA GGAGACAGGC AACATGGCCT      1200
    CACGTTTTAT GACGGATCCG CATGCGATGC GGGACATGGC GGGCCGTTTT GAGGTGCACG      1260
    CCCAGACGGT GGAGACGAG GCTCGCCGGA TGTGGGCGTC CGCGCAAAAC ATTTCCGGTG      1320
55  CGGGCTGGAG TGGCATGGCC GAGGCGACCT CGCTAGACAC CATGACCTAG ATGAATCAGG      1380
    CGTTTCGCAA CATCGTGAAC ATGCTGCACG GGGTGCCTGA CGGGCTGGTT CGCGACGCCA      1440
    ACAANTACGA ACAGCAAGAG CAGGCCTCCC AGCAGATCCT GAGCAGNTAG CGCCGAAAGC      1500
    CACAGCTGNG TACGNTTCT CACATTAGGA GAACACCAAT ATGACGATTA ATTACAGTT      1560
    CGGGGACGTC GACGCTCATG GCGCCATGAT CCGCGCTCAG GCGGCGTCGC TTGAGGCGGA      1620
60  GCATCAGGCC ATCGTTCGTG ATGTGTTGGC CGCGGGTGAC TTTTGGGGCG GCGCCGGTTC      1680
    GTTGGCTTGC CAGGAGTTCA TTACCCAGTT GGGCCGTAAC TTCCAGGTGA TCTACGAGCA      1740
    GG

```

(2) INFORMATION FOR SEQ ID NO:26: MTI (MTB9.9A)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2836 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

	GTTGATTCCG	TTCGCGGCGC	CGCCGAAGAC	CACCAACTCC	GCTGGGGTGG	TCGCACAGGC	60
	GGTTGCGTCG	GTCAGCTGGC	CGAATCCCAA	TGATTGGTGG	CTCNGTGCGG	TTGCTGGGCT	120
	CGATTACCCC	CACGGAAAGG	ACGACGATCG	TTCTGTTGCT	CGGTCAGTCG	TACTTGGCGA	180
15	CGGGCATGGC	GCGGTTTCTT	ACCTCGATCG	CACAGCAGCT	GACCTTCGGC	CCAGGGGGCA	240
	CAACGGCTGG	CTCCGGCGGA	GCCTGGTACC	CAACGCCACA	ATTCGCCGGC	CTGGGTGCAG	300
	GCCCGGCGGT	GTCGGCGAGT	TTGGCGCGGG	CGGAGCCGGT	CGGGAGGTTG	TCGGTGCCGC	360
	CAAGTTGGGC	CGTCGCGGCT	CCGGCCTTCG	CGGAGAAGCC	TGAGGCGGGC	ACGCCGATGT	420
	CCGTCATCGG	CGAAGCGTCC	AGCTGCGGTC	AGGGAGGCCT	GCTTCGAGGC	ATACCGCTGG	480
20	CGAGAGCGGG	GCGGCGTACA	GGCGCCTTCG	CTCACCAGTA	CGGGTTCGCG	CACAGCGTGA	540
	TTACCCGGTC	TCCGTCGGCG	GGATAGCTTT	CGATCCGGTC	TGCGCGGCCG	CCGGAAATGC	600
	TGCAGATAGC	GATCGACCGC	GCCGGTCGGT	AAACGCCGCA	CACGGCACTA	TCAATGCGCA	660
	CGGCGGGCGT	TGATGCCAAA	TTGACCGTCC	CGACGGGGCT	TTATCTGCGG	CAAGATTTCA	720
	TCCCCAGCCC	GGTCGGTGGG	CCGATAAATA	CGCTGCTCAG	CGCGACTCTT	CCGGCTGAAT	780
25	TCGATGCTCT	GGGCGCCCGC	TCGACGCCGA	GTATCTCGAG	TGGGCCGCAA	ACCCGGTCAA	840
	ACGCTGTTAC	TGTGGCGTTA	CCACTGGTGA	ATTTGCGGTG	CCAAGTGGTG	AACACTTGCG	900
	AACGGGTGGC	ATCGAAATCA	ACTTGTTCG	TTGCAGTGAT	CTACTCTCTT	GCAGAGAGCC	960
	GTTGCTGGGA	TTAATTGGGA	GAGGAAGACA	GCATGTCGTT	CGTGACCACA	CAGCCGGAAG	1020
	CCCTGGCAGC	TGCGGCGGCG	AACCTACAGG	GTATTGGCAC	GACAATGAAC	GCCCAGAACG	1080
30	CGGCCGCGGC	TGCTCCAACC	ACCGGAGTAG	TGCCCGCAGC	CGCCGATGAA	GTATCAGCGC	1140
	TGACCGCGGC	TCAGTTTGCT	GCGCACGCGC	AGATGTACCA	AACGGTCAGC	GCCCAGGCCG	1200
	CGGCCATTCA	CGAAATGTTT	GTGAACACGC	TGGTGGCCAG	TTCTGGCTCA	TACGCGGCCA	1260
	CCGAGGCGGC	CAACGCAGCC	GCTGCCGGCT	GAACGGGCTC	GCACGAACCT	GCTGAAGGAG	1320
	AGGGGGAACA	TCCGGAGTTC	TCCGGGTCAGG	GGTTGCGCCA	GCGCCGAGCC	GATTCAGCTA	1380
35	TCGGCGTCCA	TAACAGCAGA	CGATCTAGGC	ATTCTAGTACT	AAGGAGACAG	GCAACATGGC	1440
	CTCACGTTTT	ATGACGGATC	CGCATGCGAT	GCGGGACATG	GCGGGCCGTT	TTGAGGTGCA	1500
	CGCCAGACAG	GTGGAGGACG	AGGCTCGCCG	GATGTGGGCG	TCCGCGCAAA	ACATTTCCGG	1560
	TGCGGGCTGG	AGTGGCATGG	CCGAGGCGAC	CTCGCTAGAC	ACCATGACCT	AGATGAATCA	1620
	GGCGTTTCGC	AACATCGTGA	ACATGCTGCA	CGGGGTGCGT	GACGGGCTGG	TTCCGCGACG	1680
40	CAACAACATC	GAACAGCAAG	AGCAGGCCTC	CCAGCAGATC	CTGAGCAGCT	AGCGCCGAAA	1740
	GCCACAGCTG	CGTACGCTTT	CTCACATTAG	GAGAACACCA	ATATGACGAT	TAATTACCAG	1800
	TTCCGGGACG	TCGACGCTCA	TGGCGCCATG	ATCCGCGCTC	AGGCGCGGTC	GCTTGAGGCG	1860
	GAGCATCAGG	CCATCGTTTC	TGATGTGTTG	GCCGCGGGTG	ACTTTTGGGG	CGGCGCCGGT	1920
	TCGGTGGCTT	GCCAGGAGTT	CATTACCCAG	TTGGGCCGTA	ACTTCCAGGT	GATCTACGAG	1980
45	CAGGCCAACG	CCCACGGGCA	GAAAGTGCAG	GCTGCCGGCA	ACAACATGGC	GCAAACCGAC	2040
	AGCGCCGTCG	GCTCCAGCTG	GGCCTAAAAC	TGAACCTCAG	TCGCGGCAGC	ACACCAACCA	2100
	GCCGGTGTGC	TGCTGTGTCC	TGCAGTTAAC	TAGCACTCGA	CCGCTGAGGT	AGCGATGGAT	2160
	CAACAGAGTA	CCCCCACCAG	CATCACCGTC	AACGTCGACG	GCTTCTGGAT	GCTTCAGGCG	2220
	CTACTGGATA	TCCGCCACGT	TGCGCCTGAG	TTACGTTGCC	GGCCGTACGT	CTCCACCGAT	2280
50	TCCAATGACT	GGCTAAACGA	GCACCCGGGG	ATGGCGGTCA	TGCGCGAGCA	GGGCATTGTC	2340
	GTCAACGACG	CGGTCAACGA	ACAGGTCGCT	GCCCCGATGA	AGGTGCTTGC	CGCACCTGAT	2400
	CTTGAAGTCG	TCGCCCTGCT	GTCACGCGGC	AAGTTGCTGT	ACGGGGTCAT	AGACGACGAG	2460
	AACCAGCCGC	CGGGTTTCGCG	TGACATCCCT	GACAATGAGT	TCCGGGTGGT	GTTGGCCCCG	2520
	CGAGGCCAGC	ACTGGGTGTC	GGCGGTACGG	GTTGGCAATG	ACATCACCGT	CGATGACGTG	2580
55	ACGGTCTCGG	ATAGCGCCTC	GATCGCCGCA	CTGGTAATGG	ACGGTCTGGA	GTTCGATTAC	2640
	CACGCCGACC	CAGCCGCGAT	CAACGCGGTC	AACGTGCCAA	TGGAGGAGAT	CTCGTGCCGA	2700
	ATTTCGGCAG	AGGCACGAGG	CGGTGTCCGT	GACGACGGGA	TCGATCACGA	TCATCGACCG	2760
	GCCGGGATCC	TTGGCGATCT	CGTTGAGCAC	GACCCGGGCC	CGCGGGAAGC	TCTGCGACAT	2820
60	CCATGGGTTC	TTCCCG					2836

(2) INFORMATION FOR SEQ ID NO:27: MTI (MTB9.9A)

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

```
Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
 1      5      10      15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
      20      25      30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
      35      40      45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
      50      55      60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
      65      70      75      80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
      85      90
```

(2) INFORMATION FOR SEQ ID NO:28: HTCC#1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
35 CAGGCATGAG CAGAGCGTTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGTACG 60
ACCTTCTGGG GATTGGAATA CCCAACCAAG GGGGTATCCT TTACTCCTCA CTAGAGTACT 120
TCGAAAAAGC CCTGGAGGAG CTGGCAGCAG CGTTTCCGGG TGATGGCTGG TTAGGTTCCG 180
CCGCGGACAA ATACGCCGGC AAAAACCAGC ACCACGTGAA TTTTTCAG GAACTGGCAG 240
ACCTCGATCG TCAGCTCATC AGCCTGATCC ACGACCAGGC CAACGCGGTC CAGACGACCC 300
40 GCGACATCCT GGAGGGCGCC AAGAAAGGTC TCGAGTTCGT GCGCCCGGTG GCTGTGGACC 360
TGACCTACAT CCCGGTCGTC GGGCACGCCC TATCGGCCGC CTTCCAGGCG CCGTTTTGCG 420
CGGGCGCGAT GGCCGTAGTG GGC GGCGCGCGC TTGCCTACTT GGTCCGTGAAA ACGCTGATCA 480
ACGCGACTCA ACTCCTCAAA TTGCTTGCCA AATTGGCGGA GTTGGTCGCG GCCGCCATTG 540
CGGACATCAT TTCGGATGTG GCGGACATCA TCAAGGGCAC CCTCGGAGAA GTGTGGGAGT 600
45 TCATCACA AA CGCGCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCACG GGGTGGGTGA 660
CCGGA CTGT CTCTCGAGGG TGGTCGAACC TGGAGTCCTT CTTTGC GGGC GTCCCCGGCT 720
TGACCGGCGC GACCAGCGGC TTGTGCAAG TGA CTGGCTT GTTCGGTGCG GCCGGTCTGT 780
CCGCATCGTC GGGCTTGGCT CACGCGGATA GCCTGGCGAG CTCAGCCAGC TTGCCCCGCC 840
TGGCCGGCAT TGGGGGCGGG TCCGGTTTGT GGGGCTTGCC GAGCCTGGCT CAGGTCCATG 900
50 CCGCCTCAAC TCGGCAGGCG CTACGGCCCC GAGCTGATGG CCCGGTCGGC GCCGCTGCCG 960
AGCAGGTCGG CGGGCAGTCG CAGCTGGTCT CCGCGCAGGG TTCCCAAGGT ATGGGCGGAC 1020
CCGTAGGCAT GGGCGGCATG CACCCCTCTT CGGGGCGGTC GAAAGGGACG ACGACGAAGA 1080
AGTACTCGGA AGGCGCGGCG GCGGGCACTG AAGACGCCGA GCGCGCGCCA GTCGAAGCTG 1140
55 ACGCGGGCGG TGGGCAAAAG GTGCTGTGAC GAAACGTCGT CTAACGGCAT GGCGAGCCAA 1200
```

(2) INFORMATION FOR SEQ ID NO:29: HTCC#1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

5	Met 1	Ser	Arg	Ala	Phe 5	Ile	Ile	Asp	Pro	Thr 10	Ile	Ser	Ala	Ile	Asp 15	Gly
	Leu	Tyr	Asp	Leu	Leu	Gly	Ile	Gly	Ile	Pro	Asn	Gln	Gly	Gly	Ile	Leu
				20					25					30		
	Tyr	Ser	Ser	Leu	Glu	Tyr	Phe	Glu	Lys	Ala	Leu	Glu	Glu	Leu	Ala	Ala
10			35					40					45			
	Ala	Phe	Pro	Gly	Asp	Gly	Trp	Leu	Gly	Ser	Ala	Ala	Asp	Lys	Tyr	Ala
				50				55				60				
	Gly	Lys	Asn	Arg	Asn	His	Val	Asn	Phe	Phe	Gln	Glu	Leu	Ala	Asp	Leu
15					70						75				80	
	Asp	Arg	Gln	Leu	Ile	Ser	Leu	Ile	His	Asp	Gln	Ala	Asn	Ala	Val	Gln
					85				90						95	
	Thr	Thr	Arg	Asp	Ile	Leu	Glu	Gly	Ala	Lys	Lys	Gly	Leu	Glu	Phe	Val
20				100					105					110		
	Arg	Pro	Val	Ala	Val	Asp	Leu	Thr	Tyr	Ile	Pro	Val	Val	Gly	His	Ala
				115					120				125			
	Leu	Ser	Ala	Ala	Phe	Gln	Ala	Pro	Phe	Cys	Ala	Gly	Ala	Met	Ala	Val
25				130				135					140			
	Val	Gly	Gly	Ala	Leu	Ala	Tyr	Leu	Val	Val	Lys	Thr	Leu	Ile	Asn	Ala
					150						155				160	
	Thr	Gln	Leu	Leu	Lys	Leu	Leu	Ala	Lys	Leu	Ala	Glu	Leu	Val	Ala	Ala
30				165					170						175	
	Ala	Ile	Ala	Asp	Ile	Ile	Ser	Asp	Val	Ala	Asp	Ile	Ile	Lys	Gly	Thr
				180					185					190		
	Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	Thr	Asn	Ala	Leu	Asn	Gly	Leu	Lys
35				195				200					205			
	Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg
				210				215				220				
	Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr
40				225			230				235				240	
	Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	Thr	Gly	Leu	Phe	Gly	Ala	Ala
				245					250					255		
	Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	His	Ala	Asp	Ser	Leu	Ala	Ser
45				260				265					270			
	Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	Ile	Gly	Gly	Gly	Ser	Gly	Phe
				275				280					285			
	Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	His	Ala	Ala	Ser	Thr	Arg	Gln
50				290			295				300					
	Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	Val	Gly	Ala	Ala	Ala	Glu	Gln
					310						315				320	
	Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met
55				325					330					335		
	Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser
				340				345								

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

100


```

                260                265                270
Thr Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly
                275                280                285
5  Gly Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu
    290                295                300
Pro Glu Pro His Trp Gly Pro Phe Gly Gly Ala Ala Pro Val Ser Ala
305                310                315                320
Gly Val Gly His Ala Ala Leu Val Gly Ala Leu Ser Val Pro His Ser
                325                330                335
10 Trp Thr Thr Ala Ala Pro Glu Ile Gln Leu Ala Val Gln Ala Thr Pro
    340                345                350
Thr Phe Ser Ser Ser Ala Gly Ala Asp Pro Thr Ala Leu Asn Gly Met
    355                360                365
15 Pro Ala Gly Leu Leu Ser Gly Met Ala Leu Ala Ser Leu Ala Ala Arg
    370                375                380
Gly Thr Thr Gly Gly Gly Thr Arg Ser Gly Thr Ser Thr Asp Gly
385                390                395                400
Gln Glu Asp Gly Arg Lys Pro Pro Val Val Val Ile Arg Glu Gln Pro
                405                410                415
20 Pro Pro Gly Asn Pro Pro Arg
    420

```

(2) INFORMATION FOR SEQ ID NO:32: ESAT-6

```

25  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 154 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
30  (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```

```

35  ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA      60
    AATGTCACGT CCATTCATTC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA      120
    GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC                                154

```

(2) INFORMATION FOR SEQ ID NO:33: ESAT-6

```

40  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 51 amino acids
    (B) TYPE: amino acid
    (C) STRANDEDNESS: single
45  (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```

```

50  Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
    1      5      10      15
    Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
    20      25      30
    Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
    35      40      45
55  Glu Ala Tyr
    50

```

(2) INFORMATION FOR SEQ ID NO:34: Tb38-1

```

60  (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 327 base pairs
    (B) TYPE: nucleic acid
    (C) STRANDEDNESS: single
65  (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

```


Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 35 40 45
 Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
 50 55 60
 Pro Arg
 65

(2) INFORMATION FOR SEQ ID NO:38: 38 kD

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

20	TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTTC TCCTCGCCGA	60
	AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCTGGG GGACGTCAAG GACGCCAAGC	120
	GCGGAAATTG AAGAGCACAG AAAGGTATGG CGTGAAATT CGTTGCATA CGCTGTTGGC	180
25	CGTGTTGACC GCTGCGCCGC TGCTGCTAGC AGCGGCGGGC TGTGGCTCGA AACCACCGAG	240
	CGTTTCGCCT GAAACGGGCG CCGGCGCCCG TACTGTCTCG ACTACCCCG CGTCGTCTGCC	300
30	GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTCAACC TGTGGGGTCC	360
	GGCCTTTCAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGGTGC	420
	CGGGATCGCG CAGGCCGCGC CCGGGACGGT CAACATTGGG GCCTCCGACG CCTATCTGTC	480
35	GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGCTAGCCA TCTCCGCTCA	540
	GCAGGTCAAC TACAACCTGC CCGGAGTGAG CGAGCACCTC AAGTGAAACG GAAAAGTCCT	600
40	GGCGGCCATG TACCAGGGCA CCATCAAAAC CTGGGACGAC CCGCAGATCG CTGCGCTCAA	660
	CCCCGGCGTG AACCTGCCCC GCACCGCGGT AGTTCCGCTG CACCGCTCCG ACGGGTCCGG	720
	TGACACCTTC TTGTTCAACC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC	780
45	GCCCCGCTTC GGCACCACCG TCGACTTCCC GGCGGTGCCG GGTGCGCTGG GTGAGAACGG	840
	CAACGGCGGC ATGGTGACCG GTTGCGCCGA GACACCGGGC TGCCTGGCCT ATATCGGCAT	900
50	CAGCTTCCTC GACCAGGCCA GTCAACGGGG ACTCGGCGAG GCCCAACTAG GCAATAGCTC	960
	TGGCAATTC TTGTTGCCCG ACGCGCAAAG CATTCAAGCC GCGGCGGCTG GCTTCGCATC	1020
	GAAAACCCCG GCGAACCAGG CGATTTTCAT GATCGACGGG CCCGCCCCGG ACGGCTACCC	1080
55	GATCATCAAC TACGAGTACG CCATCGTCAA CAACCGGCAA AAGGACGCCG CCACCGCGCA	1140
	GACCTTGCAG GCATTTCTGC ACTGGGCGAT CACCGACGGC AACAAGGCCT CGTTCCTCGA	1200
60	CCAGGTTTCAT TTCCAGCCGC TGCCGCCCCG GGTGGTGAAG TTGTCTGACG CGTTGATCGC	1260
	GACGATTTC AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCGTC GGGCCATCGG	1320
	GCTGCTTTGC GGAGCATGCT GGCCCGTGCC GGTGAAGTCG GCCGCGCTGG CCCGGCCATC	1380
65	CGGTGGTTGG GTGGGATAGG TGCGGTGATC CCGCTGCTTG CGCTGGTCTT GGTGCTGGTG	1440
	GTGCTGGTCA TCGAGGCGAT GGGTGCGATC AGGCTCAACG GGTTGCATTT CTTACCGCC	1500

```

ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTCGCCCATC 1560
CGGTGCGGCG CTACTACGGG GCGTTGCCGC TGATCGTCGG GACGCTGGCG ACCTCGGCAA 1620
5 TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC 1680
TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCTGGA ATTGCTCGCC GGAATCCCCA 1740
10 GCGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG 1800
CTCCGGTGAT CGCTCACAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC 1860
CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTT GCGGGTGATG GTCGTTCCCA 1920
15 TTATCGCCAC CACCACTCAT GACCTGTTC GGCAGGTGCC GGTGTTGCCC CGGGAGGGCG 1980
CGATCGGGAA TTC 1993

```

(2) INFORMATION FOR SEQ ID NO:39: 38 kD

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1          5          10          15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20          25          30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35          40          45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50          55          60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65          70          75          80
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
85          90          95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100          105          110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115          120          125
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130          135          140
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
145          150          155          160
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
165          170          175
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
180          185          190
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
195          200          205

```


Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 5 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 10 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 15 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 20 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 25 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 30 Ile Ala Thr Ile Ser Ser
 370
 35 (2) INFORMATION FOR SEQ ID NO:40: DPEP
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 999 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
 45 ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA 60
 CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG 120
 CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCCTCG 180
 CCGCCGTCGA CCGCTGCAGC GCCACCCGCA CCGCGGACAC CTGTTGCCCC CCCACCACCG 240
 GCGCGCGCCA ACACGCCGAA TGCCAGCCG GCGGATCCCA ACGCAGCACC TCCGCCGGCC 300
 50 GACCCGAACG CACCGCCGCC ACCTGTCAAT GCCCAAACG CACCCCAACC TGTCCGGATC 360
 GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC 420
 GCCCCACTTC ACTACGGTTC AGCACTCCTC AGCAAAACCA CCGGGGACCC GCCATTTCCC 480
 GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAAG 540
 CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG 600
 55 GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC 660
 GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG 720
 CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGGCGAACGC ACCGGACGCC 780
 GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG 840
 GCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCGGGCGCCG 900
 60 GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCG CCGGGGAAGT CGCTCCTACC 960
 CCGACGACAC CGACACCGCA GCGACCTTA CCGGCCTGA 999

65 (2) INFORMATION FOR SEQ ID NO:41: DPEP
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

5
Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1 5 10 15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20 25 30
10 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35 40 45
Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50 55 60
15 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65 70 75 80
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85 90 95
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100 105 110
20 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Phe Ser
115 120 125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130 135 140
25 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145 150 155 160
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165 170 175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180 185 190
30 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195 200 205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210 215 220
35 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225 230 235 240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
245 250 255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260 265 270
40 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275 280 285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290 295 300
45 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305 310 315 320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325 330

50 (2) INFORMATION FOR SEQ ID NO:42: TbH4

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

60 CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC 60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCG CGATGCCGGC 120
ATGAACGGGC GGCATCAAT TAGTGAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT 180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG 240
AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC 300
65 CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTGTCCG 360
CCGACAACAT GCGGAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGCGT CTGGCGACCT 420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG 480
ACAACGACGG CGAAGGAAC GTGCAGGCAG AATCGGCCG GGCCGTCGGA GGGGACAGTT 540

CGGCCGAAC T AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC 600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG 660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG 702

5

(2) INFORMATION FOR SEQ ID NO:43: TbH4

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

15

Gly	Asp	Ser	Phe	Trp	Ala	Ala	Ala	Asp	Gln	Met	Ala	Arg	Gly	Phe	Val
1				5					10					15	
Leu	Gly	Ala	Thr	Ala	Gly	Arg	Thr	Thr	Leu	Thr	Gly	Glu	Gly	Leu	Gln
			20					25					30		
His	Ala	Asp	Gly	His	Ser	Leu	Leu	Asp	Ala	Thr	Asn	Pro	Ala	Val	
		35					40				45				
Val	Ala	Tyr	Asp	Pro	Ala	Phe	Ala	Tyr	Glu	Ile	Gly	Tyr	Ile	Xaa	Glu
		50				55					60				
Ser	Gly	Leu	Ala	Arg	Met	Cys	Gly	Glu	Asn	Pro	Glu	Asn	Ile	Phe	Phe
		65			70				75					80	
Tyr	Ile	Thr	Val	Tyr	Asn	Glu	Pro	Tyr	Val	Gln	Pro	Pro	Glu	Pro	Glu
			85					90						95	
Asn	Phe	Asp	Pro	Glu	Gly	Val	Leu	Gly	Gly	Ile	Tyr	Arg	Tyr	His	Ala
			100					105					110		
Ala	Thr	Glu	Gln	Arg	Thr	Asn	Lys	Xaa	Gln	Ile	Leu	Ala	Ser	Gly	Val
		115					120					125			
Ala	Met	Pro	Ala	Ala	Leu	Arg	Ala	Ala	Gln	Met	Leu	Ala	Ala	Glu	Trp
		130				135					140				
Asp	Val	Ala	Ala	Asp	Val	Trp	Ser	Val	Thr	Ser	Trp	Gly	Glu	Leu	Asn
		145			150					155				160	
Arg	Asp	Gly	Val	Val	Ile	Glu	Thr	Glu	Lys	Leu	Arg	His	Pro	Asp	Arg
			165					170						175	
Pro	Ala	Gly	Val	Pro	Tyr	Val	Thr	Arg	Ala	Leu	Glu	Asn	Ala	Arg	Gly
			180				185						190		
Pro	Val	Ile	Ala	Val	Ser	Asp	Trp	Met	Arg	Ala	Val	Pro	Glu	Gln	Ile
		195					200					205			
Arg	Pro	Trp	Val	Pro	Gly	Thr	Tyr	Leu	Thr	Leu	Gly	Thr	Asp	Gly	Phe
		210				215					220				
Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Gly	Arg	Arg	Tyr	Phe	Asn	Thr	Asp
		225			230					235				240	
Ala	Glu	Ser	Gln	Val	Gly	Arg	Gly	Phe	Gly	Arg	Gly	Trp	Pro	Gly	Arg
			245					250						255	
Arg	Val	Asn	Ile	Asp	Pro	Phe	Gly	Ala	Gly	Arg	Gly	Pro	Pro	Ala	Gln
			260				265					270			
Leu	Pro	Gly	Phe	Asp	Glu	Gly	Gly	Leu	Arg	Pro	Xaa	Lys			
		275					280				285				

45

50

(2) INFORMATION FOR SEQ ID NO:44: DPPD

55

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

60

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

65

ATGAAGTTGA	AGTTTGCTCG	CCTGAGTACT	GCGATACTGG	GTTGTGCAGC	GGCGCTTGTG	60
TTTCCTGCCT	CGGTTGCCAG	CGCAGATCCA	CCTGACCCGC	ATCAGCCGGA	CATGACGAAA	120
GGCTATTGCC	CGGGTGGCCG	ATGGGGTTTT	GGCGACTTGG	CCGTGTGCGA	CGGCGAGAAG	180

TACCCCGACG GCTCGTTTTG GCACCAAGTGG ATGCAAACGT GGTTTACCGG CCCACAGTTT 240
TACTTCGATT GTGTCAGCGG CGGTGAGCCC CTCCCCGGCC CGCCGCCACC GGGTGGTTGC 300
GGTGGGGCAA TTCCGTCCGA GCAGCCCAAC GCTCCCTGA 339

5

(2) INFORMATION FOR SEQ ID NO:45: DPPD

(i) SEQUENCE CHARACTERISTICS:

10

(A) LENGTH: 112 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
1 5 10 15
20 Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
20 25 30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
35 40 45
25 Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
50 55 60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
65 70 75 80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
85 90 95
30 Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
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35 <210> SEQ ID NO:46

<211> 921

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence:tri-fusion
protein DPV-MTI-MSL (designated Mtb31f)

40 <222> (1)..(900)

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His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
1 5 10 15

45 acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat 96
Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
20 25 30

50 ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat 144
Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
35 40 45

55 ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc 192
Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
50 55 60

60 gcg caa ttg caa gct gtg ccg ggg gcg gca cag tac atc ggc ctt gtc 240
Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
65 70 75 80

gag tgc gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat 288
Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
85 90 95

65 tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag 336
Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
100 105 110

	gcg gcg tcg ctt gag gcg gcg cat cag gcc atc gtt cgt gat gtg ttg	384
	Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu	
	115 120 125	
5	gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg gct tgc cag gag	432
	Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu	
	130 135 140	
10	ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc	480
	Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala	
	145 150 155 160	
15	aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gcg caa	528
	Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln	
	165 170 175	
20	acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg	576
	Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu	
	180 185 190	
25	gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gcg ttt gcc gcc	624
	Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala	
	195 200 205	
30	aag gcg ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gcg gcg	672
	Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala	
	210 215 220	
35	atg tcg gct cag gcg ttt cac cag ggg gag tcg tcg gcg gcg ttt cag	720
	Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln	
	225 230 235 240	
40	gcc gcc cat gcc cgg ttt gtg gcg gcg gcc gcc aaa gtc aac acc ttg	768
	Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu	
	245 250 255	
45	ttg gat gtc gcg cag gcg aat ctg ggt gag gcc gcc ggt acc tat gtg	816
	Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val	
	260 265 270	
50	gcc gcc gat gct gcg gcc gcg tcg acc tat acc ggg ttc gat atc cat	864
	Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His	
	275 280 285	
55	cac act ggc gcc cgc tcg agc aga tcc ggc tgc taacaaggcc cgaaaggaag	917
	His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys	
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60	ctga	921
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	<211> 299	
	<212> PRT	
	<213> Artificial Sequence	
	<223> Description of Artificial Sequence:tri-fusion	
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	1 5 10 15	
65	Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp	
	20 25 30	
	Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr	
	35 40 45	

5	ttg	cgc	aat	ttc	ctc	gcc	gca	ccg	cca	cct	cag	cgc	gct	gcc	atg	gcc	192
	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro	Gln	Arg	Ala	Ala	Met	Ala	
	50						55					60					
	gcg	caa	ttg	caa	gct	gtg	ccg	ggg	gcg	gca	cag	tac	atc	ggc	ctt	gtc	240
	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala	Gln	Tyr	Ile	Gly	Leu	Val	
	65					70					75					80	
10	gag	tcg	gtt	gcc	ggc	tcc	tgc	aac	aac	tat	gag	ctc	atg	acg	att	aat	288
	Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr	Glu	Leu	Met	Thr	Ile	Asn	
					85					90					95		
15	tac	cag	ttc	ggg	gac	gtc	gac	gct	cat	ggc	gcc	atg	atc	cgc	gct	cag	336
	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	
				100					105					110			
20	gcg	gcg	tcg	ctt	gag	gcg	gag	cat	cag	gcc	atc	gtt	cgt	gat	gtg	ttg	384
	Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val	Leu	
	115							120					125				
25	gcc	gcg	ggt	gac	ttt	tgg	ggc	ggc	gcc	ggt	tcg	gtg	gct	tgc	cag	gag	432
	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln	Glu	
	130						135					140					
	ttc	att	acc	cag	ttg	ggc	cgt	aac	ttc	cag	gtg	atc	tac	gag	cag	gcc	480
	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu	Gln	Ala	
	145					150					155					160	
30	aac	gcc	cac	ggg	cag	aag	gtg	cag	gct	gcc	ggc	aac	aac	atg	gcg	caa	528
	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln	
				165					170					175			
35	acc	gac	agc	gcc	gtc	ggc	tcc	agc	tgg	gcc	act	agt	atg	agc	ctt	ttg	576
	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala	Thr	Ser	Met	Ser	Leu	Leu	
				180					185					190			
40	gat	gct	cat	atc	cca	cag	ttg	gtg	gcc	tcc	cag	tcg	gcg	ttt	gcc	gcc	624
	Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser	Ala	Phe	Ala	Ala	
	195						200					205					
45	aag	gcg	ggg	ctg	atg	cgg	cac	acg	atc	ggt	cag	gcc	gag	cag	gcg	gcg	672
	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	
	210						215					220					
	atg	tcg	gct	cag	gcg	ttt	cac	cag	ggg	gag	tcg	tcg	gcg	gcg	ttt	cag	720
	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	
	225					230					235					240	
50	gcc	gcc	cat	gcc	cgg	ttt	gtg	gcg	gcg	gcc	gcc	aaa	gtc	aac	acc	ttg	768
	Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	
				245					250					255			
55	ttg	gat	gtc	gcg	cag	gcg	aat	ctg	ggg	gag	gcc	gcc	ggg	acc	tat</		

5	gtg	gcc	gcg	gag	ttg	act	tcc	gcc	gcg	gtc	tcg	tat	gga	tcg	gtg	gtg	1008	
	Val	Ala	Ala	Glu	Leu	Thr	Ser	Ala	Ala	Val	Ser	Tyr	Gly	Ser	Val	Val		
	325					330					335							
	tcg	acg	ctg	atc	gtt	gag	ccg	tgg	atg	ggg	ccg	gcg	gcg	gcc	gcg	atg	1056	
	Ser	Thr	Leu	Ile	Val	Glu	Pro	Trp	Met	Gly	Pro	Ala	Ala	Ala	Ala	Met		
	340					345					350							
10	gcg	gcc	gcg	gca	acg	ccg	tat	gtg	ggg	tgg	ctg	gcc	gcc	acg	gcg	gcg	1104	
	Ala	Ala	Ala	Ala	Thr	Pro	Tyr	Val	Gly	Trp	Leu	Ala	Ala	Thr	Ala	Ala		
	355					360					365							
15	ctg	gcg	aag	gag	acg	gcc	aca	cag	gcg	agg	gca	gcg	gcg	gaa	gcg	ttt	1152	
	Leu	Ala	Lys	Glu	Thr	Ala	Thr	Gln	Ala	Arg	Ala	Ala	Ala	Glu	Ala	Phe		
	370					375					380							
20	ggg	acg	gcg	ttc	gcg	atg	acg	gtg	cca	cca	tcc	ctc	gtc	gcg	gcc	aac	1200	
	Gly	Thr	Ala	Phe	Ala	Met	Thr	Val	Pro	Pro	Ser	Leu	Val	Ala	Ala	Asn		
	385					390					395					400		
25	cgc	agc	cgg	ttg	atg	tcg	ctg	gtc	gcg	gcg	aac	att	ctg	ggg	caa	aac	1248	
	Arg	Ser	Arg	Leu	Met	Ser	Leu	Val	Ala	Ala	Asn	Ile	Leu	Gly	Gln	Asn		
	405					410					415							
	agt	gcg	gcg	atc	gcg	gct	acc	cag	gcc	gag	tat	gcc	gaa	atg	tgg	gcc	1296	
	Ser	Ala	Ala	Ile	Ala	Ala	Thr	Gln	Ala	Glu	Tyr	Ala	Glu	Met	Trp	Ala		
	420					425					430							
30	caa	gac	gct	gcc	gtg	atg	tac	agc	tat	gag	ggg	gca	tct	gcg	gcc	gcg	1344	
	Gln	Asp	Ala	Ala	Val	Met	Tyr	Ser	Tyr	Glu	Gly	Ala	Ser	Ala	Ala	Ala		
	435					440					445							
35	tcg	gcg	ttg	ccg	ccg	ttc	act	cca	ccc	gtg	caa	ggc	acc	ggc	ccg	gcc	1392	
	Ser	Ala	Leu	Pro	Pro	Phe	Thr	Pro	Pro	Val	Gln	Gly	Thr	Gly	Pro	Ala		
	450					455					460							
40	ggg	ccc	gcg	gcc	gca	gcc	gcg	gcg	acc	caa	gcc	gcc	ggt	gcg	ggc	gcc	1440	
	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Ala	Thr	Gln	Ala	Ala	Gly	Ala	Gly	Ala		
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45	gtt	gcg	gat	gca	cag	gcg	aca	ctg	gcc	cag	ctg	ccc	ccg	ggg	atc	ctg	1488	
	Val	Ala	Asp	Ala	Gln	Ala	Thr	Leu	Ala	Gln	Leu	Pro	Pro	Gly	Ile	Leu		
	485					490					495							
	agc	gac	att	ctg	tcc	gca	ttg	gcc	gcc	aac	gct	gat	ccg	ctg	aca	tcg	1536	
	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala	Asn	Ala	Asp	Pro	Leu	Thr	Ser		
	500					505					510							
50	gga	ctg	ttg	ggg	atc	gcg	tcg	acc	ctc	aac	ccg	caa	gtc	gga	tcc	gct	1584	
	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser	Ala		
	515					520					525							
55	cag	ccg	ata	gtg	atc	ccc	acc	ccg	ata	ggg	gaa	ttg	gac	gtg	atc	gcg	1632	
	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile	Ala		
	530					535					540							
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	gag	ccg	cac	tgg	ggc	ccc	ttc	ggg	ggc	gcg	gcg	ccg	gtg	tcc	gcg	ggc	1824
	Glu	Pro	His	Trp	Gly	Pro	Phe	Gly	Gly	Ala	Ala	Pro	Val	Ser	Ala	Gly	
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5	gtc	ggc	cac	gca	gca	tta	gtc	gga	gcg	ttg	tcg	gtg	ccg	cac	agc	tgg	1872
	Val	Gly	His	Ala	Ala	Leu	Val	Gly	Ala	Leu	Ser	Val	Pro	His	Ser	Trp	
		610					615					620					
10	acc	acg	gcc	gcc	ccg	gag	atc	cag	ctc	gcc	gtt	cag	gca	aca	ccc	acc	1920
	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro	Thr	
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15	ttc	agc	tcc	agc	gcc	ggc	gcc	gac	ccg	acg	gcc	cta	aac	ggg	atg	ccg	1968
	Phe	Ser	Ser	Ser	Ala	Gly	Ala	Asp	Pro	Thr	Ala	Leu	Asn	Gly	Met	Pro	
					645					650					655		
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	Ala	Gly	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Ser	Leu	Ala	Ala	Arg	Gly	
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25	acg	acg	ggc	ggc	ggc	acc	cgt	agc	ggc	acc	agc	act	gac	ggc	caa		2064
	Thr	Thr	Gly	Gly	Gly	Thr	Arg	Ser	Gly	Thr	Ser	Thr	Asp	Gly	Gln		
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30	gag	gac	ggc	cgc	aaa	ccc	ccg	gta	gtt	gtg	att	aga	gag	cag	ccg	ccg	2112
	Glu	Asp	Gly	Arg	Lys	Pro	Pro	Val	Val	Val	Ile	Arg	Glu	Gln	Pro	Pro	
		690					695					700					
35	ccc	gga	aac	ccc	ccg	cgg	taagatttct	aaatccatca	cactggcggc	cgctcgag							2168
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50	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala	Ala	Leu	Asn	Ala	Thr	Asp	
				20					25					30			
55	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser	Pro	Val	Ala	Gln	Ser	Tyr	
			35					40					45				
60	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro	Gln	Arg	Ala	Ala	Met	Ala	
		50				55						60					
65	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala	Gln	Tyr					

	Phe 145	Ile	Thr	Gln	Leu	Gly 150	Arg	Asn	Phe	Gln	Val 155	Ile	Tyr	Glu	Gln	Ala 160
5	Asn	Ala	His	Gly 165	Gln	Lys	Val	Gln	Ala	Ala 170	Gly	Asn	Asn	Met	Ala 175	Gln
	Thr	Asp	Ser	Ala 180	Val	Gly	Ser	Ser	Trp 185	Ala	Thr	Ser	Met	Ser 190	Leu	Leu
10	Asp	Ala	His 195	Ile	Pro	Gln	Leu	Val 200	Ala	Ser	Gln	Ser	Ala 205	Phe	Ala	Ala
	Lys	Ala	Gly 210	Leu	Met	Arg	His 215	Thr	Ile	Gly	Gln	Ala 220	Glu	Gln	Ala	Ala
15	Met	Ser	Ala	Gln	Ala	Phe 230	His	Gln	Gly	Glu	Ser 235	Ser	Ala	Ala	Phe	Gln 240
20	Ala	Ala	His	Ala	Arg 245	Phe	Val	Ala	Ala	Ala 250	Ala	Lys	Val	Asn	Thr 255	Leu
	Leu	Asp	Val 260	Ala	Gln	Ala	Asn	Leu	Gly 265	Glu	Ala	Ala	Gly	Thr 270	Tyr	Val
25	Ala	Ala	Asp 275	Ala	Ala	Ala	Ala	Ser 280	Thr	Tyr	Thr	Gly	Phe 285	Asp	Ile	Met
	Asp	Phe	Gly 290	Leu	Leu	Pro	Pro 295	Glu	Val	Asn	Ser	Ser 300	Arg	Met	Tyr	Ser
30	Gly	Pro	Gly 305	Pro	Glu	Ser 310	Met	Leu	Ala	Ala	Ala 315	Ala	Ala	Trp	Asp	Gly 320
	Val	Ala	Ala	Glu	Leu	Thr 325	Ser	Ala	Ala	Val 330	Ser	Tyr	Gly	Ser	Val 335	Val
35	Ser	Thr	Leu 340	Ile	Val	Glu	Pro	Trp	Met 345	Gly	Pro	Ala	Ala 350	Ala	Ala	Met
	Ala	Ala	Ala 355	Ala	Thr	Pro	Tyr	Val 360	Gly	Trp	Leu	Ala	Ala 365	Thr	Ala	Ala
40	Leu	Ala	Lys 370	Glu	Thr	Ala	Thr 375	Gln	Ala	Arg	Ala	Ala 380	Ala	Glu	Ala	Phe
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	Arg	Ser	Arg	Leu	Met 405	Ser	Leu	Val	Ala	Ala 410	Asn	Ile	Leu	Gly	Gln 415	Asn
50	Ser	Ala	Ala	Ile 420	Ala	Ala	Thr	Gln	Ala 425	Glu	Tyr	Ala	Glu 430	Met	Trp	Ala
	Gln	Asp	Ala 435	Ala	Val	Met	Tyr	Ser 440	Tyr	Glu	Gly	Ala 445	Ser	Ala	Ala	Ala
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	Val	Ala	Asp	Ala	Gln	Ala 485	Thr	Leu	Ala	Gln	Leu 490	Pro	Pro	Gly	Ile 495	Leu
65	Ser	Asp	Ile	Leu	Ser	Ala	Leu	Ala	Ala 505	Asn	Ala	Asp	Pro	Leu	Thr	Ser

	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser	Ala	
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5	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile	Ala	
		530					535					540					
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	545					550					555					560	
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					565					570					575		
	Leu	Gly	Pro	Thr	Gln	Gly	His	Pro	Leu	Ser	Ser	Ala	Thr	Asp	Glu	Pro	
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	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro	Thr	
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			675					680						685			
35	Glu	Asp	Gly	Arg	Lys	Pro	Pro	Val	Val	Val	Ile	Arg	Glu	Gln	Pro	Pro	
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	Pro	Gly	Asn	Pro	Pro	Arg											
40		705				710											